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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
08/973,363	02/04/1998	RICHARD GRIFFITHS	263PPNTIR117	6817

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EXAMINER
SCHNIZER, RICHARD A

ART UNIT	PAPER NUMBER
1635	

DATE MAILED: 10/17/2002

29

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.	Applicant(s)
08/973,363	Griffiths
Examiner	**Art Unit**
Richard Schnizer	1635

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136 (a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1) [X] Responsive to communication(s) filed on *Aug 15, 2002*.

2a) [ ] This action is **FINAL**. 2b) [X] This action is non-final.

3) [ ] Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11; 453 O.G. 213.

Disposition of Claims

4) [X] Claim(s) *34-56* is/are pending in the application.

4a) Of the above, claim(s) *50-54* is/are withdrawn from consideration.

5) [X] Claim(s) *55 and 56* is/are allowed.

6) [X] Claim(s) *34-49* is/are rejected.

7) [ ] Claim(s) _____ is/are objected to.

8) [ ] Claims _____ are subject to restriction and/or election requirement.

Application Papers

9) [ ] The specification is objected to by the Examiner.

10) [ ] The drawing(s) filed on _____ is/are a) [ ] accepted or b) [ ] objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11) [ ] The proposed drawing correction filed on _____ is: a) [ ] approved b) [ ] disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12) [ ] The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13) [X] Acknowledgement is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a) [X] All b) [ ] Some* c) [ ] None of:

1. [ ] Certified copies of the priority documents have been received.
2. [ ] Certified copies of the priority documents have been received in Application No. _____.
3. [X] Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

*See the attached detailed Office action for a list of the certified copies not received.

14) [ ] Acknowledgement is made of a claim for domestic priority under 35 U.S.C. § 119(e).

a) [ ] The translation of the foreign language provisional application has been received.

15) [ ] Acknowledgement is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) [X] Notice of References Cited (PTO-892)
2) [ ] Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) [ ] Information Disclosure Statement(s) (PTO-1449) Paper No(s). _____
4) [ ] Interview Summary (PTO-413) Paper No(s). _____
5) [ ] Notice of Informal Patent Application (PTO-152)
6) [ ] Other:

DETAILED ACTION

Continued Examination Under 37 CFR 1.114

A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on 7/18/02 has been entered.

An amendment containing Figures 12-17 was received and entered as Paper No. 28 on 8/15/02.

Claims 55 and 56 were added as requested in Paper No. 27, filed 7/18/02.

Claims 34-56 are pending.

Claims 50-54 were withdrawn from consideration in Paper No. 15 as being drawn to a non-elected invention.

Claims 34-49, 55, and 56 are under consideration in this Office Action.

Compliance with Sequence Rules

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the

following reason(s). Applicant's attention is directed to the final rule making notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998). Nucleic acid sequences in excess of 9 nucleotides are disclosed in the specification at page 18, lines 12-14 and page 19, lines 23 and 24, but these sequences are not identified by any SEQ ID NO. An amino sequences in excess of three amino acids are disclosed at page 32, lines 25 and 26, but these sequences are not identified by any SEQ ID NO. Originally filed Figs 1, 3, 5, and 7-11 also disclose nucleic acid or amino acid sequences which are not identified by SEQ ID NOS. It is noted that Applicant submitted Figures in Paper No. 6, filed March 9, 1998, which were in compliance with the Sequence Rules. However, because these Figures were not accompanied by any amendment directed their entry into the specification, the original Figures have not been replaced. Finally, although a CRF in compliance with the Sequence Rules has been filed, the Application lacks a paper copy of the Sequence Listing. Furthermore, it is not clear that the current CRF lists the sequences on pages 8, 19, and 32 described above.

Applicant must provide:

A substitute computer readable form (CRF) copy of the "Sequence Listing".

An initial paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

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Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Written Description

Claims 34-49 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are drawn to isolated polynucleotides comprising sequences derived from a CHD gene of a bird. The sequences may comprise any of SEQ ID NOS: 1-5, 10, 12, or 15, or may encode the polypeptides of SEQ ID NOS: 6-9, 11, or 14. These claims read on full length cDNAs and genomic clones encoding any bird CHD gene. In analyzing whether the written description requirement is met for genus claims, it is first determined whether a representative number of species has been described by complete structure, such as nucleotide sequence, next it is determined whether a representative number of species has been described by other relevant identifying characteristics, such as a common structural feature shared by all the members of the claimed genus.

The specification discloses various genomic and cDNA fragments of CHD genes from the mouse and from two birds, but fails to disclose any full-length cDNA of any bird CHD gene, any full-length genomic clone of any bird CHD gene, any common sequence which is shared by all the members of the claimed genus, nor any sequence characteristic which identifies any sequence as having been derived from a bird rather than from some other animal. The specification indicates that all birds are believed to have two or more CHD type genes, one W-linked, and one either autosomal or Z-linked. See page 4, lines 1-8. Because the specification discloses sequences from only two birds, but all birds are expected to have CHD-genes, the claimed genus is considered to embrace an enormous number of sequences which have yet to be discovered. Because the disclosed sequences do not include any full-length genomic or cDNA

clones, and include no sequence identified as common to all the members of the genus, the disclosed sequences do not constitute a substantial portion of the claimed genus.

Weighing the available evidence, i.e. the lack of disclosure of full-length cDNA or genomic clones, the breadth of the claims which clearly encompasses such sequences from any bird, and the failure to identify any sequence common to all of the members of the genus, one of skill in the art could not conclude that Applicant was in possession of the claimed genus at the time of filing.

Enablement

Claims 35, 37, 39, 41, 43, 45, and 47-49 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for isolated nucleotide sequences consisting of SEQ ID NOS: 1-5, 10, 12, 13, or 15, does not reasonably provide enablement for other nucleic acids such as full length cDNAs or genomic clones of bird CHD genes. Also the specification, while enabling for methods of determining the sex of a non-ratite bird, or its cells, tissues or a nonratite bird fetus, comprising hybridizing nucleic at least one of SEQ ID NOS: 1-5, 10, 12, 13, or 15 to a DNA derived from the bird, tissue , cell or fetus, wherein the DNA has been digested with a restriction enzyme that allows one to distinguish between CHD-W and CHD1-A genes, does not reasonably provide enablement for such hybridization methods in which the target DNA has not been digested with a restriction enzyme that allows one to distinguish between CHD-W and CHD1-A genes. Finally, the specification does not reasonably

provide enablement for sequences comprising SEQ ID NOS: 1-5, 10, 12, 13, or 15, or encoding the amino acid sequences of SEQ ID NOS: 6-9, 11, or 14, which hybridize only to the W chromosome, and not to any other chromosome. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

Claims 35, 37, 39, 41, 43, 45, and 47-49 are drawn to nucleic acid sequences which comprise nucleic acids encoding the polypeptide sequences of SEQ ID NOS: 6-9, 11, and 14 which give a W-specific signal upon hybridization to nucleic acids from any bird.

Hybridization between two nucleic acids can be thought of as occurring between a probe sequence and a target sequence. Applicant has described the amino acid sequences of SEQ ID NOS: 6-9, 11 11, and 14, and it is well within the ability of one of skill in the art to determine all of

the nucleic acid sequences which could encode these amino acid sequences. Thus Applicant has taught a wide variety of probe sequences. However, Applicant has not taught which of these sequences can be used in the invention. For example, if one were to make a probe by changing every wobble base in SEQ ID NO:2, which encodes a mouse CHD-11 gene, the resulting probe sequence would be about 67% identical to SEQ ID NO:2 and would be encompassed by the claims. SEQ ID NO:2 is about 80% identical to the chicken CHD-lA gene, and CHD-lA is about 90% identical to CHD-W. See page 23, lines 5 and 6, and page 25, lines 19-21. Thus it seems reasonable that the probe would be about 50% identical to the W-specific CHD-W target

sequence. Under the hybridization conditions disclosed at page 9, lines 13-16 of the specification, one would not expect such a probe to hybridize to the target sequence at all. Furthermore, Applicant has not taught any target sequence other than chicken and great tit sequences, and there is no guidance in the prior art of record as to the sequence of any target nucleic acids not disclosed in the specification. Thus there appears to be no way to accurately predict which of the described probes will be useful for generating a W-specific sequence in birds other than the chicken or the great tit. For these reasons, one of skill in the art would be unable to select appropriate probes from the described genus, and would be unable to use the claimed sequences invention commensurate in scope with the claims without undue experimentation.

Claims 48 and 49 are specifically drawn to a method of determining the sex of a non-ratite bird by hybridization of the nucleic acids of claims 34, 35, 42, or 43 to DNA isolated from the bird. The recited nucleic acids are homologous to the CHD-1A and CHD-W genes which Applicant has shown to be conserved in at least 13 species of widely disparate birds. Both genes are transcribed into RNA, however the specification does not appear to teach how to distinguish between the RNAs transcribed from these two genes. No information is presented with respect to differences in the sizes or tissue distribution of the two classes of RNAs, so it is unclear how any claimed nucleic acid could be made or used to provide a W-specific signal could be generated by hybridization with the claimed sequences.

The specification provides convincing evidence that SEQ ID NOS: 1-5, 10, 12, 13, and 15 can be used to yield a W-specific signal when the DNAs of the subject bird have been digested with the restriction enzyme Dde I. Digestion with Dde I is performed because the claimed nucleic acids hybridize to both autosomal-specific (CHD-1A) and W-specific (CHD-W) avian sequences, thus some method of differentiating between CHD-1A and CHD-W signals is required. For example, the specification teaches that PCR amplification of genomic DNA from a variety of birds gives fragments of precisely the same length which correspond to both CHD-1A and CHD-W sequences. Digestion with a restriction endonuclease which recognizes CHD-W nucleic acids allows one to distinguish the CHD-W signal from the CHD-1A signal. The specification teaches no method other than restriction digestion which can be used to distinguish these signals. For this reason, the claimed nucleic acids could not be used to provide a W-specific signal when applied to non-condensed chromosomal DNA in situ, or to DNA which has not been, or will not be, digested with a restriction endonuclease that allows separation of fragments of diagnostic sizes. Furthermore, armed with the teachings of the specification, one of skill in the art could not make any claimed sequence which could be used to do so. Because the specification does not teach how to distinguish between hybridization signals from CHD-W and CHD1-A targets by any means other than by the size of restriction fragments, and there is no other readily apparent means for distinguishing these signals for the reasons discussed above, one of skill in the art would have to perform undue experimentation to practice the invention by any other means. This portion of the rejection could be overcome by incorporating a restriction

digestion step into the method, wherein the restriction digestion yielded hybridizable fragments of CHD-W which were of a different size than those of CHD1-A.

Claims 36-41 require polynucleotides that give a specific signal only on the W chromosome upon hybridization to genomic DNA of a non-ratite bird. The specification shows unambiguously that these claims are not enabled because it teaches that the disclosed sequences of the CHD-W and CHD1-A genes are at least 90.5% identical. See page 25, lines 19 and 21. The hybridization conditions disclosed in the specification allow hybridization between sequences that are 90% identical. See page 9, lines 13-15. For this reason, any disclosed sequence that will hybridize to bird genomic DNA under the disclosed hybridization conditions will hybridize to both CHD-W and CHD1-A. For this reason one of skill in the art could not make the claimed invention without undue experimentation.

Response to Arguments

Applicant's arguments filed 7/18/02 (Paper No. 27) and 8/15/02 (Paper No. 28) have been fully considered as they apply to the grounds of rejection set forth above but they are not persuasive.

Applicant argues at paragraph three, page 7 of Paper No. 27 that the ground of rejection relating to accurately predicting which of the claimed sequences will be useful for generating a W-specific sequence is unfounded because the claim requires that the sequences must be hybridizable to the genomic DNA of a bird. This is unpersuasive because the specification does

not teach which sequences have this characteristic. Furthermore, the claim sets forth no conditions under which the hybridization occurs. The specificity of hybridization clearly decreases with decreasing stringency. Under low enough stringency conditions, the claimed sequences will hybridize with many sequences in birds that are autosomal. The specification does not teach how to distinguish these signals from those arising from hybridization to W-chromosome sequences.

The rejection of claims 48 and 49 is discussed at pages 7 and 8 of Paper No. 27, and pages 2-7 of Paper No. 28. Applicant's arguments regarding the use of antibodies to detect CHD-W polypeptides are confusing. The claims require determination of sex by detection of nucleic acid hybridization. It is unclear how Applicant intends to use anti-CHD-W antibodies to detect nucleic acid hybridization, and in any event, the specification fails to teach how to do so.

Applicant argues at page 8 of Paper No. 27 that the specification teaches methods other than restriction digest can be used, relying for support on page 12, lines 15-28, page 13, lines 10-24, page 14, lines 1-16, page 20, lines 5-6, page 21, lines 8-15, page 25, lines 15-24, and page 26, lines 7-16. The first of these passages discloses a PCR method. This portion of the argument is unpersuasive because the claimed method does not allow for detection by PCR. Note the methods allow hybridization with only one polynucleotide. Furthermore, the claims are drawn to polynucleotides that will recognize only one strand of a duplex. Clearly PCR requires oligonucleotides complementary to each strand. One of ordinary skill in the art appreciates that two oligonucleotides are required for PCR. Reliance on the passage at page 25, lines 15-24 is

unpersuasive because this passage discloses no hybridization technique. All of the other passages, as well as Figures 12 and 13, refer to Southern blots, Clearly these passages fall within the scope **indicated in the rejection to be enabled** because Southern blotting requires restriction digestion.

At pages 4-7 of Paper No. 28, Applicant makes more PCR-based arguments. These are unpersuasive for the reasons set forth above, i.e. the claims do not allow for detection by PCR because they allow for hybridization with only one polynucleotide.

At page 5 of Paper No. 28, Applicant asserts that the method cold be performed by hybridization to chromosome spreads. The Examiner acknowledges that this technique should be applicable to preparations of condensed chromosomes which are morphologically distinguishable. However, the claims are not limited to hybridization to condensed, morphologically distinguishable chromosomes but embrace the entire genus of detection techniques based on hybridization with a single probe. The vast majority of these techniques are not enabled because they fail to provide any means of distinguishing between hybridization to CHD1-A and CHD-W. The Examiner has not indicated that hybridization to condensed chromosomes is part of the enabled scope of the invention because no literal support for this technique could be found in the specification, thus amendment of the claims to include this technique would result in the introduction of new matter. The indicated scope of enablement is consistent with the teachings of the specification in view of the breadth of the claims.

At page 6 of Paper No. 29, Applicant argues that SSCP could be used to distinguish between CHD1-A and CHD-W PCR products. This argument is unpersuasive because the claims require detection by hybridization, not by any other method.

For these reasons the rejection is maintained.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 34-49 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 34-49 are indefinite because they describe SEQ ID NO:2, either directly as in claims 34, 36, 38, 40, 42, 44, 46, 48, and 49, or indirectly as in claims 35, 37, 39, 41, 43, 45, and 47-49, as a polynucleotide derived from a bird. SEQ ID NO:2 is derived from a mouse.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless -

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 36, 37, and 40-47 are rejected under 35 U.S.C. 102(b) as being anticipated by Delmas et al (Proc. Nat Acad. Sci. USA 90(6): 2414-2418, 1993).

Delmas teaches a single polynucleotide with 66.7% overall homology to SEQ ID No. 2, 79.2% local homology to SEQ ID NO:3, and overall 67.2% homology to SEQ ID No.15, and shorter stretches of 100% identity with these sequences. See Fig 11, page 2415. Because the sequence of Delmas comprises segments of 100% identity with those of SEQ ID Nos. 2-5, 10, and 15, it is deemed to comprise fragments of nucleotides sequences according to claims 34 and 35, thus claims 36 and 37 are included in this rejection. The specification does not define the term "fragment" so it is given its broadest reasonable interpretation, i.e. it is considered to embrace segments of sequence. The Delmas sequence is construed as comprising segments or fragments which anticipate the claim.

Thus Delmas anticipates the claims.

Response to Arguments

Applicant's arguments filed 7/18/02 (Paper No. 27) and 8/15/02 (Paper No. 28) have been fully considered as they apply to the grounds of rejection set forth above but they are not persuasive.

Applicant argues that "moderate to high stringency" is defined as corresponding to "about at least 75% homology." This is incorrect. The specification does not define "moderate to high stringency". It defines only "moderate stringency" and "high stringency". "Moderate

stringency" is defined as "corresponding to "about 75% homology". The specification provides no definition of the term "about" in this context. Absent evidence to the contrary, the 66.7% and 67.2% identity of Delmas is "about" 75% homology. Applicant has provided no evidence to the contrary. Applicant further argues that Delmas does not teach fragments of its polynucleotide. This is unpersuasive because the polynucleotide of Delmas comprises segments of 100% identity with those of SEQ ID Nos. 2-5, 10, and 15. The specification does not explicitly preclude a "fragment" from being physically associated with other less homologous sequences. That is, the specification does not preclude fragments from being comprised within larger sequences. In other words, the term "fragment" has been given its broadest reasonable interpretation, and has been deemed to correspond to "segment". Finally, Applicant argues that Delmas teaches a mouse cDNA encoding a mouse protein, not a bird DNA encoding a bird protein. This is unpersuasive because, in terms of the nature of the claimed composition, the source of the polynucleotide and the process by which it was produced is not deemed to affect the material nature of the polynucleotide. Therefore, if a polynucleotide meets the structural requirements of a composition claim, it is identical to the composition under 35 USC 102. See MPEP 2112. Which states in part:

> "Products of identical chemical composition can not have mutually exclusive properties." A chemical composition and its properties are inseparable. Therefore, if the prior art teaches the identical chemical structure, the properties applicant discloses and/or claims are necessarily present. In re Spada, 911 F.2d 705, 709, 15 USPQ2d 1655, 1658 (Fed. Cir. 1990) (Applicant argued that the claimed composition was a pressure sensitive adhesive containing a tacky polymer while the product of the reference was hard and abrasion resistant. "The Board correctly found that the virtual identity of monomers and procedures sufficed to support a prima facie case of unpatentability of Spada's polymer latexes for lack of novelty.").

The source of the polynucleotide, and its method of isolation are irrelevant.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

Claims 36, 37, and 40-47 are rejected under 35 U.S.C. 103(a) as being unpatentable over Delmas et al (Proc. Nat Acad. Sci USA 90(6): 2414-2418, 1993) in view of Bresser et al (US Patent 5,225,326, issued 7/6/93).

Delmas teaches a single polynucleotide with 66.7% homology to SEQ ID No. 2 and 67.2% homology to SEQ ID No.15. Delmas does not teach fragments of the polynucleotide which are not covalently linked to the rest of the polynucleotide, i.e. restriction fragments, which are about 75% homologous to the claimed sequences.

Bresser teaches a one step method of *in situ* hybridization using a mixture of oligonucleotides designed to span the entire length of the target polynucleotide. For DNA probes, the oligonucleotides are generally 15-150 bases in length. If a target nucleic acid were 1000 bases long, then about 20-70 different probes of 15-150 bases would be used to completely cover the target polynucleotide. See column 10, line 68 to column 11, line 8.

It would have been obvious to use the method of Bresser to examine the expression of the sequence of Delmas by hybridization in situ in order to assess its expression in tissues in situ. One would have bee motivated to do so because Delmas was clearly interested in determining the types of cells in which the message was expressed, having performed Northern blots of various different mouse cell lines (see e.g. Fig 5 on page 2418), and because Bresser teaches that in situ hybridization allows the identification of specific cells within an animal that express a given message. See column 1, lines 51-67. In the process of executing the method of Bresser, on would have generated a variety of probes that meet the limitations of the claims. For example, bases 3909-4088 of Delmas have only 26 mismatches relative to SEQ ID NO: 15. This corresponds to a sequence identity of 89.2%. In order to cover this 180 base segment as taught by Bresser, one would have to generate some combination of probes from 15-150 bases in length, and at least some of these probes would have had to be at least 89.2% identical to SEQ ID NO:15. On the other hand, the sequence of Delmas is identical to SEQ ID NO:2 for 102 bases from position 52 to 153. In the process of covering this region with probes as taught by Bresser, one would necessarily make a variety of fragments that anticipate the claims.

Thus the invention as a whole was *prima facie* obvious.

Conclusion

Claims 55 and 56 are allowable. Claims 38 and 39 are free of the art of record.

[redacted]

Any inquiry concerning this communication or earlier communications from the examiner(s) should be directed to Richard Schnizer, whose telephone number is 703-306-5441. The examiner can normally be reached Monday through Friday between the hours of 6:20 AM and 3:50 PM. The examiner is off on alternate Fridays, but is sometimes in the office anyway.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, John Leguyader, can be reached at 703-308-0447. The FAX numbers for art unit 1632 are 703-308-4242, and 703-305-3014. Additionally correspondence can be transmitted to the following RIGHTFAX numbers: 703-872-9306 for correspondence before final rejection, and 703-872-9307 for correspondence after final rejection.

Inquiries of a general nature or relating to the status of the application should be directed to the Patent Analyst Trina Turner whose telephone number is 703-305-3413.

Richard Schnizer, Ph.D.

JAMES KETTER
PRIMARY EXAMINER